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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/905,744

DATE: 11/21/2001

TIME: 12:14:40

Input Set : N:\Crif3\RULE60\09905744.txt

Output Set: N:\CRF3\11212001\I905744.raw

3 <110> APPLICANT: Chadwick, Brian Paul  
 4 Frischauf, Anna-Maria  
 6 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO CD39-LIKE  
 7 POLYPEPTIDES AND NUCLEIC ACIDS  
 9 <130> FILE REFERENCE: 9598-066  
 11 <140> CURRENT APPLICATION NUMBER: 09/905,744  
 12 <141> CURRENT FILING DATE: 2001-07-13  
 14 <150> PRIOR APPLICATION NUMBER: 09/240,639  
 15 <151> PRIOR FILING DATE: 1999-01-29  
 17 <160> NUMBER OF SEQ ID NOS: 29  
 19 <170> SOFTWARE: PatentIn Ver. 2.0  
 21 <210> SEQ ID NO: 1  
 22 <211> LENGTH: 2762  
 23 <212> TYPE: DNA  
 24 <213> ORGANISM: Homo sapiens  
 26 <220> FEATURE:  
 27 <221> NAME/KEY: CDS  
 28 <222> LOCATION: (232)..(1599)  
 30 <400> SEQUENCE: 1

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 35 ggcgggtgca tggaatgggc tatgtgaatg aaaaaaggta tccgttatga aacttccaga 180  
 37 aaaacgagct acatttttca gcagccgcag cacggtcctt ggcaacaag g atg aga 237  
 38 Met Arg  
 39 1

41 aaa ata tcc aac cac ggg agc ctg cgg gtg gcg aag gtg gca tac ccc 285  
 42 Lys Ile Ser Asn His Gly Ser Leu Arg Val Ala Lys Val Ala Tyr Pro  
 43 5 10 15  
 45 ctg ggg ctg tgt gtg ggc gtg ttc atc tat gtt gcc tac atc aag tgg 333  
 46 Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile Lys Trp  
 47 20 25 30  
 49 cac cgg gcc acc gcc acc cag gcc ttc ttc agc atc acc agg gca gcc 381  
 50 His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg Ala Ala  
 51 35 40 45 50  
 53 cgg ggg gcc cgg tgg ggt cag cag gcc cac agc ccc ctg ggg aca gct 429  
 54 Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly Thr Ala  
 55 55 60 65  
 57 gca gac ggg cac gag gtc ttc tac ggg atc atg ttt gat gca gga agc 477  
 58 Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala Gly Ser  
 59 70 75 80  
 61 act ggc acc cga gta cac gtc ttc cag ttc acc cgg ccc ccc aga gaa 525  
 62 Thr Gly Thr Arg Val His Val Phe Gln Phe Thr Arg Pro Pro Arg Glu  
 63 85 90 95  
 65 act ccc acg tta acc cac gaa acc ttc aaa gca gtg aag cca ggt ctt 573  
 66 Thr Pro Thr Leu Thr His Glu Thr Phe Lys Ala Val Lys Pro Gly Leu  
 67 100 105 110  
 69 tct gcc tat gct gat gat gtt gaa aag agc gct cag gga atc cgg gaa 621

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70 Ser Ala Tyr Ala Asp Asp Val Glu Lys Ser Ala Gln Gly Ile Arg Glu
71 115 120 125 130
73 cta ctg gat gtt gct aaa cag gac att ccg ttc gac ttc tgg aag gcc 669
74 Leu Leu Asp Val Ala Lys Gln Asp Ile Pro Phe Asp Phe Trp Lys Ala
75 135 140 145
77 acc cct ctg gtc ctc aag gcc aca gct ggc tta cgc ctg tta cct gga 717
78 Thr Pro Leu Val Leu Lys Ala Thr Ala Gly Leu Arg Leu Leu Pro Gly
79 150 155 160
81 gaa aag gcc cag aag tta ctg cag aag gtg aaa gaa gta ttt aaa gca 765
82 Glu Lys Ala Gln Lys Leu Leu Gln Lys Val Lys Glu Val Phe Lys Ala
83 165 170 175
85 tcg cct ttc ctt gta ggg gat gac tgt gtt tcc atc atg aac gga aca 813
86 Ser Pro Phe Leu Val Gly Asp Asp Cys Val Ser Ile Met Asn Gly Thr
87 180 185 190
89 gat gaa ggc gtt tcg gcg tgg atc acc atc aac ttc ctg aca ggc agc 861
90 Asp Glu Gly Val Ser Ala Trp Ile Thr Ile Asn Phe Leu Thr Gly Ser
91 195 200 205 210
93 ttg aaa act cca gga gag agc agc gtg ggc atg ctg gac ttg ggc gga 909
94 Leu Lys Thr Pro Gly Gly Ser Ser Val Gly Met Leu Asp Leu Gly Gly
95 215 220 225
97 gga tcc act cag atc gcc ttc ctg cca cgc gtg gag ggc acc ctg cag 957
98 Gly Ser Thr Gln Ile Ala Phe Leu Pro Arg Val Glu Gly Thr Leu Gln
99 230 235 240
101 gcc tcc cca ccc ggc tac ctg acg gca ctg cgg atg ttt aac agg acc 1005
102 Ala Ser Pro Pro Gly Tyr Leu Thr Ala Leu Arg Met Phe Asn Arg Thr
103 245 250 255
105 tac aag ctc tat tcc tac agc tac ctc ggg ctc ggg ctg atg tcg gca 1053
106 Tyr Lys Leu Tyr Ser Tyr Ser Tyr Leu Gly Leu Gly Leu Met Ser Ala
107 260 265 270
109 cgc ctg gcg atc ctg ggc ggc gtg gag ggg cag cct gct aag gat gga 1101
110 Arg Leu Ala Ile Leu Gly Gly Val Glu Gly Gln Pro Ala Lys Asp Gly
111 275 280 285 290
113 aag gag ttg gtc agc cct tgc ttg tct ccc agt ttc aaa gga gag tgg 1149
114 Lys Glu Leu Val Ser Pro Cys Leu Ser Pro Ser Phe Lys Gly Glu Trp
115 295 300 305
117 gaa cac gca gaa gtc acg tac agg gtt tca ggg cag aaa gca gcg gca 1197
118 Glu His Ala Glu Val Thr Tyr Arg Val Ser Gly Gln Lys Ala Ala Ala
119 310 315 320
121 agc ctg cac gag ctg tgt gct gcc aga gtg tca gag gtc ctt caa aac 1245
122 Ser Leu His Glu Leu Cys Ala Ala Arg Val Ser Glu Val Leu Gln Asn
123 325 330 335
125 aga gtg cac agg acg gag gaa gtg aag cat gtg gac ttc tat gct ttc 1293
126 Arg Val His Arg Thr Glu Glu Val Lys His Val Asp Phe Tyr Ala Phe
127 340 345 350
129 tcc tac tat tac gac ctt gca gct ggt gtg ggc ctc ata gat gcg gag 1341
130 Ser Tyr Tyr Tyr Asp Leu Ala Ala Gly Val Gly Leu Ile Asp Ala Glu
131 355 360 365 370
133 aag gga ggc agc ctg gtg gtg ggg gac ttc gag atc gca gcc aag tac 1389
134 Lys Gly Gly Ser Leu Val Val Gly Asp Phe Glu Ile Ala Ala Lys Tyr

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135          375          380          385
137 gtg tgt cgg acc ctg gag aca cag ccg cag agc agc ccc ttc tca tgc 1437
138 Val Cys Arg Thr Leu Glu Thr Gln Pro Gln Ser Ser Pro Phe Ser Cys
139          390          395          400
141 atg gac ctc acc tac gtc agc ctg cta ctc cag gag ttc ggc ttt ccc 1485
142 Met Asp Leu Thr Tyr Val Ser Leu Leu Leu Gln Glu Phe Gly Phe Pro
143          405          410          415
145 agg agc aaa gtg ctg aag ctc act cgg aaa att gac aat gtt gag acc 1533
146 Arg Ser Lys Val Leu Lys Leu Thr Arg Lys Ile Asp Asn Val Glu Thr
147          420          425          430
149 agc tgg gct ctg ggg gcc att ttt cat tac atc gac tcc ctg aac aga 1581
150 Ser Trp Ala Leu Gly Ala Ile Phe His Tyr Ile Asp Ser Leu Asn Arg
151 435          440          445          450
153 cag aag agt cca gcc tca tagtggccga gccatccctg tccccgtcag 1629
154 Gln Lys Ser Pro Ala Ser
155          455
157 cagtgtctgt gtgtctgcat aaacctcct gtccctggacg tgacttcac ctaggagacc 1689
159 acagcacagg ccgtctgggc actttctgca cactggctct gggacttgca gaaggcctgg 1749
161 tctgtccctg gcatcagcct ctccagtcga catctggcca gagggctgtc tggacctggg 1809
163 cctgtctcaa tgcacctgt ctgctgggc tccaagtggg caggaccagg acagaaccac 1869
165 aggcacacac tgagggggca gtgtggctcc ctgctgtcc catcccatg ccccgctccg 1929
167 ggggtctgtg ctgctgtgt gcatgtccct gcgatgggag tcttgtctcc cagcctgtca 1989
169 gtttccctcc cagggcagag ctcccttcc tgcaagagtc tgggaggcgg tgcaggctgt 2049
171 cctggctgct ctggggaagc cgagggacag ccataacacc cccgggacag taggtctggg 2109
173 cggcaccact gggaaactct gacttgagtg tgtttgtct tcttgggta tgaatgtgtg 2169
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183 ctgtgtcctg tgaatgtat gctactgtga gctgttccc cctagccagg gccatgtctt 2469
185 agtgcgact gtgccacgg tcagctgag cacagtccca gaaccaagct ctcggtgtct 2529
187 cgggccacca tccgccacc tcgggctgac cccacctcct ccatggacag tgtgagcccc 2589
189 gggccgtgca tctgtctcag tgtggcgta gtgtggggc tgagccccct gagctgtctc 2649
191 agtgaatgta cagtgtcccg cagagctga acctcatgtg ttccactccc aataaaaggt 2709
193 tgacaggggc ttctccttca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 2762
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199 <213> ORGANISM: Homo sapiens
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205 Tyr Pro Leu Gly Leu Cys Val Gly Val Phe Ile Tyr Val Ala Tyr Ile
206 20 25 30
208 Lys Trp His Arg Ala Thr Ala Thr Gln Ala Phe Phe Ser Ile Thr Arg
209 35 40 45
211 Ala Ala Pro Gly Ala Arg Trp Gly Gln Gln Ala His Ser Pro Leu Gly
212 50 55 60
214 Thr Ala Ala Asp Gly His Glu Val Phe Tyr Gly Ile Met Phe Asp Ala

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220	Arg	Glu	Thr	Pro	Thr	Leu	Thr	His	Glu	Thr	Phe	Lys	Ala	Val	Lys	Pro	
221				100					105					110			
223	Gly	Leu	Ser	Ala	Tyr	Ala	Asp	Asp	Val	Glu	Lys	Ser	Ala	Gln	Gly	Ile	
224			115					120					125				
226	Arg	Glu	Leu	Leu	Asp	Val	Ala	Lys	Gln	Asp	Ile	Pro	Phe	Asp	Phe	Trp	
227		130					135					140					
229	Lys	Ala	Thr	Pro	Leu	Val	Leu	Lys	Ala	Thr	Ala	Gly	Leu	Arg	Leu	Leu	
230	145					150					155				160		
232	Pro	Gly	Glu	Lys	Ala	Gln	Lys	Leu	Leu	Gln	Lys	Val	Lys	Glu	Val	Phe	
233				165						170					175		
235	Lys	Ala	Ser	Pro	Phe	Leu	Val	Gly	Asp	Cys	Val	Ser	Ile	Met	Asn		
236			180						185					190			
238	Gly	Thr	Asp	Glu	Gly	Val	Ser	Ala	Trp	Ile	Thr	Ile	Asn	Phe	Leu	Thr	
239		195						200					205				
241	Gly	Ser	Leu	Lys	Thr	Pro	Gly	Gly	Ser	Ser	Val	Gly	Met	Leu	Asp	Leu	
242		210					215					220					
244	Gly	Gly	Gly	Ser	Thr	Gln	Ile	Ala	Phe	Leu	Pro	Arg	Val	Glu	Gly	Thr	
245	225					230					235				240		
247	Leu	Gln	Ala	Ser	Pro	Pro	Gly	Tyr	Leu	Thr	Ala	Leu	Arg	Met	Phe	Asn	
248				245						250				255			
250	Arg	Thr	Tyr	Lys	Leu	Tyr	Ser	Tyr	Ser	Tyr	Leu	Gly	Leu	Gly	Leu	Met	
251			260						265					270			
253	Ser	Ala	Arg	Leu	Ala	Ile	Leu	Gly	Gly	Val	Glu	Gly	Gln	Pro	Ala	Lys	
254		275						280					285				
256	Asp	Gly	Lys	Glu	Leu	Val	Ser	Pro	Cys	Leu	Ser	Pro	Ser	Phe	Lys	Gly	
257		290					295					300					
259	Glu	Trp	Glu	His	Ala	Glu	Val	Thr	Tyr	Arg	Val	Ser	Gly	Gln	Lys	Ala	
260	305					310					315				320		
262	Ala	Ala	Ser	Leu	His	Glu	Leu	Cys	Ala	Ala	Arg	Val	Ser	Glu	Val	Leu	
263				325							330				335		
265	Gln	Asn	Arg	Val	His	Arg	Thr	Glu	Glu	Val	Lys	His	Val	Asp	Phe	Tyr	
266			340						345					350			
268	Ala	Phe	Ser	Tyr	Tyr	Tyr	Asp	Leu	Ala	Ala	Gly	Val	Gly	Leu	Ile	Asp	
269			355					360					365				
271	Ala	Glu	Lys	Gly	Gly	Ser	Leu	Val	Val	Gly	Asp	Phe	Glu	Ile	Ala	Ala	
272		370					375					380					
274	Lys	Tyr	Val	Cys	Arg	Thr	Leu	Glu	Thr	Gln	Pro	Gln	Ser	Ser	Pro	Phe	
275	385					390					395				400		
277	Ser	Cys	Met	Asp	Leu	Thr	Tyr	Val	Ser	Leu	Leu	Gln	Glu	Phe	Gly		
278				405						410				415			
280	Phe	Pro	Arg	Ser	Lys	Val	Leu	Lys	Leu	Thr	Arg	Lys	Ile	Asp	Asn	Val	
281			420						425					430			
283	Glu	Thr	Ser	Trp	Ala	Leu	Gly	Ala	Ile	Phe	His	Tyr	Ile	Asp	Ser	Leu	
284			435					440					445				
286	Asn	Arg	Gln	Lys	Ser	Pro	Ala	Ser									
287		450					455										

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299 <210> SEQ ID NO: 3
291 <211> LENGTH: 2797
292 <212> TYPE: DNA
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296 <221> NAME/KEY: CDS
297 <222> LOCATION: (83)..(1669)
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303 Met Phe Thr Val Leu Thr Arg Gln Pro Cys
304 1 5 10
306 gag caa gca ggc ctc aag gcc ctc tac cga act cca acc atc att gcc 160
307 Glu Gln Ala Gly Leu Lys Ala Leu Tyr Arg Thr Pro Thr Ile Ile Ala
308 15 20 25
310 ttg gtg gtc ttg ctt gtg agt att gtg gta ctt gtg agt atc act gtc 208
311 Leu Val Val Leu Leu Val Ser Ile Val Val Leu Val Ser Ile Thr Val
312 30 35 40
314 atc cag atc cac aag caa gag gtc ctc cct cca gga ctg aag tat ggt 256
315 Ile Gln Ile His Lys Gln Glu Val Leu Pro Pro Gly Leu Lys Tyr Gly
316 45 50 55
318 att gtg ctg gat gcc ggg tct tca aga acc aca gtc tac gtg tat caa 304
319 Ile Val Leu Asp Ala Gly Ser Ser Arg Thr Thr Val Tyr Val Tyr Gln
320 60 65 70
322 tgg cca gca gaa aaa gag aat aat acc gga gtg gtc agt caa acc ttc 352
323 Trp Pro Ala Glu Lys Glu Asn Asn Thr Gly Val Val Ser Gln Thr Phe
324 75 80 85 90
326 aaa tgt agt gtg aaa ggc tct gga atc tcc agc tat gga aat aac ccc 400
327 Lys Cys Ser Val Lys Gly Ser Gly Ile Ser Ser Tyr Gly Asn Asn Pro
328 95 100 105
330 caa gat gtc ccc aga gcc ttt gag gag tgt atg caa aaa gtc aag ggg 448
331 Gln Asp Val Pro Arg Ala Phe Glu Glu Cys Met Gln Lys Val Lys Gly
332 110 115 120
334 cag qtt cca tcc cac ctc cac gga tcc acc ccc att cac ctg gga gcc 496
335 Gln Val Pro Ser His Leu His Gly Ser Thr Pro Ile His Leu Gly Ala
336 125 130 135
338 acg gct ggg atg cgc ttg ctg agg ttg caa aat gaa aca gca gct aat 544
339 Thr Ala Gly Met Arg Leu Leu Arg Leu Gln Asn Glu Thr Ala Ala Asn
340 140 145 150
342 gaa gtc ctt gaa agc atc caa agc tac ttc aag tcc cag ccc ttt gac 592
343 Glu Val Leu Glu Ser Ile Gln Ser Tyr Phe Lys Ser Gln Pro Phe Asp
344 155 160 165 170
346 ttt agg ggt gct caa atc att tct ggg caa gaa gaa ggg gta tat gga 640
347 Phe Arg Gly Ala Gln Ile Ile Ser Gly Gln Glu Glu Gly Val Tyr Gly
348 175 180 185
350 tgg att aca gcc aac tat tta atg gga aat ttc ctg gag aag aac ctg 688
351 Trp Ile Thr Ala Asn Tyr Leu Met Gly Asn Phe Leu Glu Lys Asn Leu
352 190 195 200
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